

Blast Result

EXHIBIT Q

Blast 2 Sequences results

NCBI Entrez BLAST OMIM Taxonomy Structure

PubMed

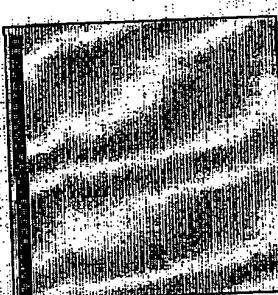
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec 14 2001]

Match: 1 Mi: mismatch: 2 gap open: 5 gap extension: 2

x dropoff: 50 expect: 10.000 wordsize: 11 Filter Align

Sequence gi 13027635 Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA Length 2753 (1..2753)

Sequence 1cl1sq_2 2



Score = 43.0 bits (22), Expect = 1.6
 Identities = 24/25 (96%)
 Strand = Plus / Minus

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 43.0 bits (22), Expect = 1.6
 Identities = 24/25 (96%)
 Strand = Plus / Minus

Query: 118 ctacacaaaaagcgtggatcactca 142

Sbjct: 25 cttaacaaaaagcttggatcactca 1

CPU time: 0.06 user secs. 0.05 sys. secs. 0.11 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped Lambda K H
 1.33 0.621 1.12

Matrix: blast1 matrix: 1 -2
 Gap Penalties: Existence: 5 Extension: 2
 Number of Hits to DB: 1

3/8/2002

Blast Result

Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
length of query: 2753
length of database: 5,006,917,935
effective HSP length: 95
effective length of query: 2728
effective length of database: 5,006,452,710
effective search space: 13641234992880
effective search space used: 13641234992880
T: 0
A: 3.0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)